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FIG. 1A-1

Mtt1	793SQIFITNIAAGGREIKVIK.E.....CP
Upf1	547ADVVCCTCVGAGDKRIDT...K....ER
Sen1	1413	DRDEMREKNSVYNRDLDRRNAQAHI ^{LAVSDIICSTLSGSAHDVIA} TMGIK.....FD
Dip1	351FKTIKDIIQSRIVVTTLHGSSSRELCSLYRDDPNFQLEFD
Dna2	1128	KHKVHPDTQKYVPNYASVKSYNDYLSKINSTSVATTCLGI.NDILFTLNED.....FD
consensus	241	l s i v t t i g r l t i k f d
Mtt1	816	VVMDEATQSSEASTVPI ^{SLPGIR..NEVFVGDEKQLSSFSNIIP}QLE
Upf1	568	TVLIDESIQASEPECLIPI.VKCAK.QVILVGDHQQLG.....PVILERKAADA..GLK
Sen1	1467	TVIDEACQCTELSSIPIRY.GGK.RCIMVGDPNQL.....PPTVLSGAASNF..KYN
Dip1	391	TLLIDEVSQAMEPCWCWIPLIAHQNQFHKLVLADGNKQL.....PPTIKTEDDDKNVIHNL
Dna2	1182	YVIDEASQISMFAVALGPRIY...GNRFIMVGDHVYL.....PPLVKNDAAAR..LGGLE
consensus	301	tviideatq sep lipl g r r ilvgd ql pp i a le
Mtt1	862	TSLFERRVLSNGTYKNFLM.LDTQYRMHEKI SEFFIKKIYNGEL
Upf1	618	QSLFERLISLGHV..PIR.LEVQYRMNPYLSEFPSPMFYEGL
Sen1	1517	QSLFVRMEKN...SSPYL.LDVQYRMHPSISKFPSSSEFYQGRI
Dip1	446	TTLFDRRIKIFPKRDMVKFLNVQYRMNQKIMEFPSHSMYNCKILLADATVANRLLDLP TV
Dna2	1231	ESLFKTFCCEKHPS.VAELTLQYRMCGDIUTLSNFLIYDNKLCGNNNEVFAQSLELPMP
consensus	361	sLFervl pl ldvQYRM p ifefps iYngri
Mtt1	904
Upf1	658
Sen1	1556
Dip1	506	DA.....
Dna2	1289	EALSRYNESANSKQWLEDILEPTRKVVFVNVDNCPDIEQSEKDNITNHGEAELTLQCV
consensus	421

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FIG. 1B

Mtt1	904KDGVTDEQKA.....	WPGVQH.....	PLFFYQCDIGFESR	
Upf1	658QNGVTIEQRTVPNSKFPPIRGI		FMFW.ANYGRE..	
Sen1	1556KDG.....	PGMDILNKRPHWQLEPLAPYKFFDIISGRQ..		
Dip1	508TPSED.....	DDDTKIPLIWD.TQGDFFQ		
Dna2	1349	EGMLLSGVPCED.....			
consensus	481	dg	p	pl fy	g e
Mtt1	934	VRSTQRDIVGFTYE.....	NKHECVEIVKIIQIILMLDKKVPLE...EI		
Upf1	692	...EISANGTSFL.....	NRIEAMNCERIIITKILFRDGVKP.E...QI		
Sen1	1589	...EQNAKTMSYT.....	NMEIRVAIELVDYLFRKFDNKIDFTGKI		
Dip1	532	ETADEATILGSKYNEGEIAIVKEHLENLRSNVEE		NSI	
Dna2	1361			I
consensus	541	e g ty	n e	ii l	e l
Mtt1	974	GVITPYSACQRDILSDILTKNVVINPKQISMQQEYDEIELFNAAGSQGTAGSLQNNVINII			
Upf1	727	GVITPYEGQRAYILOYMOMN.....		GSIDK...DLY	
Sen1	1628	GIISPYREQ.....		MQMRKEFARYFGGMINKS.....	
Dip1	570	GVI SPYNAQVSHLKKLIHDELKLTID.....			
Dna2	1362	GVTILYRAQLRIILKKIFNKIV.....			Y
consensus	601	Gvitpy aQ l il nv			g l
Mtt1	1034	NGLHVATVDSEFGHEKSEFIIFSCVRN.NTENKIGFIRDKRRINVALTRAK~			
Upf1	755	IKVEVASVDAFQGREKDYIILSCVRA.NEQQAIGFIRDERRLNVGLTRAK~			
Sen1	1656	..IDENIIDCFQCGQKEIILISCVRADDTKSSVGFKDFRRANVALTRAK~			
Dip1	595	..IEISTVDGFQGREKDYIILSVRS.NEKFEVGFLEERRLNVAITRPR~			
Dna2	1384	DGLEILTADQFGQDKKCIILISVVRNSQLNGGAILLEIRHVNVAITRKS			
consensus	661	lev tvDaFQGreKd iilScvR n n igfLkd RRINValTRak			